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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,254

DATE: 07/16/2002 P-6
TIME: 14:01:35

Input Set : A:\Sequence Listing 1321.2.29.1.txt

Output Set: N:\CRF3\07162002\J009254.raw

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3 <110> APPLICANT: University of Utah Research Foundation
4      Adderson, Elisabeth
5      Bohnsack, John
7 <120> TITLE OF INVENTION: Isolated Genes for Virulent Group B Streptococcus agalactiae
9 <130> FILE REFERENCE: 1321.2.29
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/009,254
C--> 11 <141> CURRENT FILING DATE: 2001-12-10
11 <150> PRIOR APPLICATION NUMBER: 60/140,084
12 <151> PRIOR FILING DATE: 1999-06-21
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1509
20 <212> TYPE: DNA
21 <213> ORGANISM: Streptococcus agalactiae
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1509)
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29 Met Lys Lys Lys Met Ile Gln Ser Leu Leu Val Ala Ser Leu Ala Phe
30 1      5      10      15
32 ggt atg gct gta tca cca gtt acg ccg ata gct ttt gcc gct gag aca      96
33 Gly Met Ala Val Ser Pro Val Thr Pro Ile Ala Phe Ala Ala Glu Thr
34      20      25      30
36 ggg aca att aca gtt caa gat act caa aaa ggc gca acc tat aaa gca      144
37 Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
38      35      40      45
40 tat aaa gtt ttt gat gca gaa ata gat aat gca aat gta tct gat tcg      192
41 Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
42      50      55      60
44 aat aaa gat gga gct tct tat tta att cct caa ggt aaa gaa gct gag      240
45 Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
46 65      70      75      80
48 tat aaa gct tca act gat ttt aat tct ctt ttt acg aca act act aat      288
49 Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Asn
50      85      90      95
52 gga ggg aga aca tat gta act aaa aaa gat act gcg tca gca aat gag      336
53 Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
54      100      105      110
56 att gcg aca tgg gct aaa tct ata tca gct aat act aca cca gtt tcc      384
57 Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
58      115      120      125

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60	act	gtt	act	gag	tca	aat	aat	gat	ggt	act	gag	gtt	att	aat	gtt	tcc	432
61	Thr	Val	Thr	Glu	Ser	Asn	Asn	Asp	Gly	Thr	Glu	Val	Ile	Asn	Val	Ser	
62		130					135				140						
64	caa	tat	gga	tat	tat	tat	gtt	tct	agc	act	gtt	aat	aat	gga	gct	gta	480
65	Gln	Tyr	Gly	Tyr	Tyr	Tyr	Val	Ser	Ser	Thr	Val	Asn	Asn	Gly	Ala	Val	
66	145					150				155					160		
68	att	atg	gtt	aca	tct	gta	act	cca	aat	gct	act	att	cat	gaa	aag	aat	528
69	Ile	Met	Val	Thr	Ser	Val	Thr	Pro	Asn	Ala	Thr	Ile	His	Glu	Lys	Asn	
70					165					170					175		
72	act	gat	gcg	aca	tgg	gga	gat	ggt	ggt	gga	aaa	act	gta	gat	caa	aaa	576
73	Thr	Asp	Ala	Thr	Trp	Gly	Asp	Gly	Gly	Lys	Thr	Val	Asp	Gln	Lys		
74			180					185					190				
76	acg	tac	tcg	gtt	ggt	gat	aca	gtc	aaa	tat	act	att	act	tat	aag	aat	624
77	Thr	Tyr	Ser	Val	Gly	Asp	Thr	Val	Lys	Tyr	Thr	Ile	Thr	Tyr	Lys	Asn	
78			195				200				205						
80	gca	gtc	aat	tat	cat	ggt	aca	gaa	aaa	gtg	tat	caa	tat	gtt	ata	aag	672
81	Ala	Val	Asn	Tyr	His	Gly	Thr	Glu	Lys	Val	Tyr	Gln	Tyr	Val	Ile	Lys	
82		210				215				220							
84	gat	act	atg	cca	tct	gct	tct	gta	gtt	gat	ttg	aac	gaa	ggg	tct	tat	720
85	Asp	Thr	Met	Pro	Ser	Ala	Ser	Val	Val	Asp	Leu	Asn	Glu	Gly	Ser	Tyr	
86	225				230					235					240		
88	gaa	gta	act	att	act	gat	gga	tca	ggg	aat	att	aca	act	cta	act	caa	768
89	Glu	Val	Thr	Ile	Thr	Asp	Gly	Ser	Gly	Asn	Ile	Thr	Thr	Leu	Thr	Gln	
90			245					250					255				
92	ggt	tcg	gaa	aaa	gca	act	ggg	aag	tat	aac	ctg	tta	gag	gaa	aat	aat	816
93	Gly	Ser	Glu	Lys	Ala	Thr	Gly	Lys	Tyr	Asn	Leu	Leu	Glu	Glu	Asn	Asn	
94			260					265					270				
96	aat	ttc	acg	att	act	att	ccg	tgg	gca	gct	acc	aat	act	cca	acc	gga	864
97	Asn	Phe	Thr	Ile	Thr	Ile	Pro	Trp	Ala	Ala	Thr	Asn	Thr	Pro	Thr	Gly	
98		275				280					285						
100	aat	act	caa	aat	gga	gct	aat	gat	gac	ttt	ttt	tat	aag	gga	ata	aat	912
101	Asn	Thr	Gln	Asn	Gly	Ala	Asn	Asp	Asp	Phe	Phe	Tyr	Lys	Gly	Ile	Asn	
102		290				295				300							
104	aca	atc	aca	gtc	act	tat	aca	gga	gta	tta	aag	agt	gga	gct	aaa	cca	960
105	Thr	Ile	Thr	Val	Thr	Tyr	Thr	Gly	Val	Leu	Lys	Ser	Gly	Ala	Lys	Pro	
106	305				310					315					320		
108	ggt	tca	gct	gat	tta	cca	gaa	aat	aca	aac	att	gcg	acc	atc	aac	ccc	1008
109	Gly	Ser	Ala	Asp	Leu	Pro	Glu	Asn	Thr	Asn	Ile	Ala	Thr	Ile	Asn	Pro	
110			325					330				335					
112	aat	act	agc	aat	gat	gac	cca	ggt	caa	aaa	gta	aca	gtg	agg	gat	ggt	1056
113	Asn	Thr	Ser	Asn	Asp	Asp	Pro	Gly	Gln	Lys	Val	Thr	Val	Arg	Asp	Gly	
114			340					345				350					
116	caa	att	act	ata	aaa	aaa	att	gat	ggt	tcc	aca	aaa	gct	tca	tta	caa	1104
117	Gln	Ile	Thr	Ile	Lys	Lys	Ile	Asp	Gly	Ser	Thr	Lys	Ala	Ser	Leu	Gln	
118		355				360					365						
120	ggt	gct	ata	ttt	gtt	tta	aag	aat	gct	acg	ggt	caa	ttt	cta	aac	ttt	1152
121	Gly	Ala	Ile	Phe	Val	Leu	Lys	Asn	Ala	Thr	Gly	Gln	Phe	Leu	Asn	Phe	
122		370				375					380						
124	aac	gat	aca	aat	aac	gtt	gaa	tgg	ggc	aca	gaa	gct	aat	gca	aca	gaa	1200

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126 385                      390                      395                      400
128 tat aca aca gga gca gat ggt ata att acc att aca ggc ttg aaa gaa      1248
129 Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
130                      405                      410                      415
132 ggt aca tac tat cta gtt gag aaa aag gct ccc tta ggt tac aat ttg      1296
133 Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
134                      420                      425                      430
136 tta gat aac tct cag aag gtt att tta gga gat gga gcc act gat acg      1344
137 Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
138                      435                      440                      445
140 act aat tca gat aac ctt tta gtt aac cca act gtt gaa aat aac aaa      1392
141 Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
142                      450                      455                      460
144 ggt act gag ttg cct tca aca ggt ggt att ggt aca aca att ttc tac      1440
145 Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
146 465                      470                      475                      480
148 att ata ggt gca att tta gta ata gga gca ggt atc gtg ctt gtt gct      1488
149 Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala
150                      485                      490                      495
152 cgt cgt cgt tta cgt tct taa      1509
153 Arg Arg Arg Leu Arg Ser
154                      500
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 502
159 <212> TYPE: PRT
160 <213> ORGANISM: Streptococcus agalactiae
162 <400> SEQUENCE: 2
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169                      20                      25                      30
172 Gly Thr Ile Thr Val Gln Asp Thr Gln Lys Gly Ala Thr Tyr Lys Ala
173                      35                      40                      45
176 Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
177                      50                      55                      60
180 Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
181 65                      70                      75                      80
184 Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Thr Asn
185                      85                      90                      95
188 Gly Gly Arg Thr Tyr Val Thr Lys Lys Asp Thr Ala Ser Ala Asn Glu
189                      100                     105                     110
192 Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
193                      115                     120                     125
196 Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser
197                      130                     135                     140
200 Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
201 145                     150                     155                     160
204 Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn

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205          165          170          175
208 Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val Asp Gln Lys
209          180          185          190
212 Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
213          195          200          205
216 Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
217          210          215          220
220 Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
221 225          230          235          240
224 Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
225          245          250          255
228 Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn
229          260          265          270
232 Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
233          275          280          285
236 Asn Thr Gln Asn Gly Ala Asn Asp Asp Phe Phe Tyr Lys Gly Ile Asn
237          290          295          300
240 Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
241 305          310          315          320
244 Gly Ser Ala Asp Leu Pro Glu Asn Thr Asn Ile Ala Thr Ile Asn Pro
245          325          330          335
248 Asn Thr Ser Asn Asp Asp Pro Gly Gln Lys Val Thr Val Arg Asp Gly
249          340          345          350
252 Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
253          355          360          365
256 Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
257          370          375          380
260 Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
261 385          390          395          400
264 Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
265          405          410          415
268 Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu
269          420          425          430
272 Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr
273          435          440          445
276 Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
277          450          455          460
280 Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
281 465          470          475          480
284 Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala
285          485          490          495
288 Arg Arg Arg Leu Arg Ser
289          500
292 <210> SEQ ID NO: 3
293 <211> LENGTH: 1692
294 <212> TYPE: DNA
295 <213> ORGANISM: Streptococcus agalactiae
297 <220> FEATURE:
298 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING

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299 <222> LOCATION: (1)..(1692)
301 <400> SEQUENCE: 3
302 att tgc att atg gtg atc gta ttc cgg att ata cag ata tta caa ggg      48
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304 1          5          10          15
306 att ata tcc aag atc ctt cag gta cat att att ata agt atg att cac      96
307 Ile Ile Ser Lys Ile Leu Gln Val His Ile Ile Ile Ser Met Ile His
308          20          25          30
310 gag ata aag atc ccg act caa cta aag atg cct att ata cga cag ata      144
311 Glu Ile Lys Ile Pro Thr Gln Val Lys Met Pro Ile Ile Arg Gln Ile
312          35          40          45
314 cta gtc tca tca aat gtt gat aca aca act aag tac aag tac gta aaa      192
315 Leu Val Ser Ser Asn Val Asp Thr Thr Thr Lys Tyr Lys Tyr Val Lys
316          50          55          60
318 gac gct tac aaa tta gtc ggt tgg tat tat gtt aat cca tat ggt agt      240
319 Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser
320 65          70          75          80
322 att aga cct tat aac ttt tca ggt gct gta act caa gat atc aat tta      288
323 Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu
324          85          90          95
326 aga gct att tgg cga aag gct gga gat tat cat att ata tac agc aat      336
327 Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn
328          100          105          110
330 gat gct gtt ggt aca gat gga aag cca gca ttg gat gct tct ggt cag      384
331 Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln
332          115          120          125
334 caa tta caa aca agt aat gag cct act gac cct gat tcc tat gac gat      432
335 Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp
336          130          135          140
338 ggc tcc cat tca gcc tta ctg aga cgt ccg aca atg cca gat ggc tat      480
339 Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr
340 145          150          155          160
342 cgt ttc cgt ggc tgg tgg tac aat ggt aaa att tat aac cca tat gat      528
343 Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp
344          165          170          175
346 tcc att gat att gac gcc cat tta gca gat gct aat aaa aat atc acc      576
347 Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr
348          180          185          190
350 ata aaa cct gtc att att cca gta gga gat atc aaa tta gaa gat acc      624
351 Ile Lys Pro Val Ile Ile Pro Val Gly Asp Ile Lys Leu Glu Asp Thr
352          195          200          205
354 tcc atc aaa tac aat ggt aac ggt ggt act aga gta gaa aat ggt aat      672
355 Ser Ile Lys Tyr Asn Gly Asn Gly Gly Thr Arg Val Glu Asn Gly Asn
356          210          215          220
358 gtg gta aca caa gtg gag aca ccg cgt atg gag ttg aat agc aca act      720
359 Val Val Thr Gln Val Gln Thr Pro Arg Met Glu Leu Asn Ser Thr Thr
360 225          230          235          240
362 aca att cct gaa aac caa tac ttt aca agg aca ggt tac aac ctt att      768
363 Thr Ile Pro Glu Asn Gln Tyr Phe Thr Arg Thr Gly Tyr Asn Leu Ile

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 3

VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing 1321.2.29.1.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:655 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9

L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0